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RAW SEQUENCE LISTING

DATE: 05/08/2001

PATENT APPLICATION: US/09/835,082

TIME: 11:28:37

Input Set : A:\ARCD349USC1.txt

Output Set: N:\CRF3\05082001\I835082.raw

ENTERED

3 <110> APPLICANT: RATAIN, MARK J.
 4 INNOCENTI, FEDERICO
 5 IYER, LALITHA
 7 <120> TITLE OF INVENTION: FLAVOPIRIDOL DRUG COMBINATIONS AND METHODS WITH
 8 REDUCED SIDE EFFECTS
 10 <130> FILE REFERENCE: ARCD:349USC1
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/835,082
 13 <141> CURRENT FILING DATE: 2001-04-12
 15 <160> NUMBER OF SEQ ID NOS: 4
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 2320
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (19)..(1611)
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 31 1 5 10
 33 cta tgt gtg tgt ctg ctg ctg acc tgt ggc ttt gcc gag gca ggg aag 99
 34 Leu Cys Val Cys Leu Leu Leu Thr Cys Gly Phe Ala Glu Ala Gly Lys
 35 15 20 25
 37 cta ctg gta gtg ccc atg gat ggg agc cac tgg ttc acc atg agg tgc 147
 38 Leu Leu Val Val Pro Met Asp Gly Ser His Trp Phe Thr Met Arg Ser
 39 30 35 40
 41 gtg gtg gag aaa ctc att ctc agg ggg cat gag gtg gtt gta gtc atg 195
 42 Val Val Glu Lys Leu Ile Leu Arg Gly His Glu Val Val Val Met
 43 45 50 55
 45 cca gag gtg agt tgg caa ctg gga aga tca ctg aat tgc aca gtg aag 243
 46 Pro Glu Val Ser Trp Gln Leu Gly Arg Ser Leu Asn Cys Thr Val Lys
 47 60 65 70 75
 49 act tat tca act tca tat acc ctg gag gat ctg gac cgg gag ttc aag 291
 50 Thr Tyr Ser Thr Ser Tyr Thr Leu Glu Asp Leu Asp Arg Glu Phe Lys
 51 80 85 90
 53 gct ttt gcc cat gct caa tgg aaa gca caa gta cga agt ata tat tct 339
 54 Ala Phe Ala His Ala Gln Trp Lys Ala Gln Val Arg Ser Ile Tyr Ser
 55 95 100 105
 57 cta tta atg ggt tca tac aat gac att ttt gac tta ttt ttt tca aat 387
 58 Leu Leu Met Gly Ser Tyr Asn Asp Ile Phe Asp Leu Phe Phe Ser Asn
 59 110 115 120
 61 tgc agg agt ttg ttt aaa gac aaa aaa tta gta gaa tac tta aag gag 435
 62 Cys Arg Ser Leu Phe Lys Asp Lys Lys Leu Val Glu Tyr Leu Lys Glu
 63 125 130 135
 65 agt tct ttt gat gca gtg ttt ctc gat cct ttt gat aac tgt ggc tta 483
 66 Ser Ser Phe Asp Ala Val Phe Leu Asp Pro Phe Asp Asn Cys Gly Leu

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67 140      145      150      155
69 att gtt gcc aaa tat ttc tcc ctc ccc tcc gtg gtc ttc gcc agg gga 531
70 Ile Val Ala Lys Tyr Phe Ser Leu Pro Ser Val Val Phe Ala Arg Gly
71      160      165      170
73 ata ctt tgc cac tat ctt gaa gaa ggt gca cag tgc cct gct cct ctt 579
74 Ile Leu Cys His Tyr Leu Glu Glu Gly Ala Gln Cys Pro Ala Pro Leu
75      175      180      185
77 tcc tat gtc ccc aga att ctc tta ggg ttc tca gat gcc atg act ttc 627
78 Ser Tyr Val Pro Arg Ile Leu Leu Gly Phe Ser Asp Ala Met Thr Phe
79      190      195      200
81 aag gag aga gta cgg aac cac atc atg cac ttg gag gaa cat tta tta 675
82 Lys Glu Arg Val Arg Asn His Ile Met His Leu Glu Glu His Leu Leu
83      205      210      215
85 tgc cac cgt ttt ttc aaa aat gcc cta gaa ata gcc tct gaa att ctc 723
86 Cys His Arg Phe Phe Lys Asn Ala Leu Glu Ile Ala Ser Glu Ile Leu
87 220      225      230      235
89 caa aca cct gtt acg gag tat gat ctc tac agc cac aca tca att tgg 771
90 Gln Thr Pro Val Thr Glu Tyr Asp Leu Tyr Ser His Thr Ser Ile Trp
91      240      245      250
93 ttg ttg cga acg gac ttt gtt ttg gac tat ccc aaa ccc gtg atg ccc 819
94 Leu Leu Arg Thr Asp Phe Val Leu Asp Tyr Pro Lys Pro Val Met Pro
95      255      260      265
97 aac atg atc ttc att ggt ggt atc aac tgc cat cag gga aag ccg ttg 867
98 Asn Met Ile Phe Ile Gly Gly Ile Asn Cys His Gln Gly Lys Pro Leu
99      270      275      280
101 cct atg gaa ttt gaa gcc tac att aat gct tct gga gaa cat gga att 915
102 Pro Met Glu Phe Glu Ala Tyr Ile Asn Ala Ser Gly Glu His Gly Ile
103      285      290      295
105 gtg gtt ttc tct ttg gga tca atg gtc tca gaa att cca gag aag aaa 963
106 Val Val Phe Ser Leu Gly Ser Met Val Ser Glu Ile Pro Glu Lys Lys
107 300      305      310      315
109 gct atg gca att gct gat gct ttg ggc aaa atc cct cag aca gtc ctg 1011
110 Ala Met Ala Ile Ala Asp Ala Leu Gly Lys Ile Pro Gln Thr Val Leu
111      320      325      330
113 tgg cgg tac act gga acc cga cca tgc aat ctt gcg aac aac acg ata 1059
114 Trp Arg Tyr Thr Gly Thr Arg Pro Ser Asn Leu Ala Asn Asn Thr Ile
115      335      340      345
117 ctt gtt aag tgg cta ccc caa aac gat ctg ctt ggt cac ccg atg acc 1107
118 Leu Val Lys Trp Leu Pro Gln Asn Asp Leu Leu Gly His Pro Met Thr
119      350      355      360
121 cgt gcc ttt atc acc cat gct ggt tcc cat ggt gtt tat gaa agc ata 1155
122 Arg Ala Phe Ile Thr His Ala Gly Ser His Gly Val Tyr Glu Ser Ile
123      365      370      375
125 tgc aat ggc gtt ccc atg gtg atg atg ccc ttg ttt ggt gat cag atg 1203
126 Cys Asn Gly Val Pro Met Val Met Met Pro Leu Phe Gly Asp Gln Met
127 380      385      390      395
129 gac aat gca aag cgc atg gag act aag gga gct gga gtg acc ctg aat 1251
130 Asp Asn Ala Lys Arg Met Glu Thr Lys Gly Ala Gly Val Thr Leu Asn
131      400      405      410

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133 gtt ctg gaa atg act tct gaa gat tta gaa aat gct cta aaa gca gtc 1299
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135 415 420 425
137 atc aat gac aaa agt tac aag gag aac atc atg cgc ctc tcc agc ctt 1347
138 Ile Asn Asp Lys Ser Tyr Lys Glu Asn Ile Met Arg Leu Ser Ser Leu
139 430 435 440
141 cac aag gac cgc ccg gtg gag ccg ctg gac ctg gcc gtg ttc tgg gtg 1395
142 His Lys Asp Arg Pro Val Glu Pro Leu Asp Leu Ala Val Phe Trp Val
143 445 450 455
145 gag ttt gtg atg agg cac aag ggc gcg cca cac ctg cgc ccc gca gcc 1443
146 Glu Phe Val Met Arg His Lys Lys Ala Pro His Leu Arg Pro Ala Ala
147 460 465 470 475
149 cac gac ctc acc tgg tac cag tac cat tcc ttg gac gtg att ggt ttc 1491
150 His Asp Leu Thr Trp Tyr Gln Tyr His Ser Leu Asp Val Ile Gly Phe
151 480 485 490
153 ctc ttg gcc gtc gtg ctg aca gtg gcc ttc atc acc ttt aaa tgt tgt 1539
154 Leu Leu Ala Val Val Leu Thr Val Ala Phe Ile Thr Phe Lys Cys Cys
155 495 500 505
157 gct tat ggc tac cgg aaa tgc ttg ggg aaa aaa ggg cga gtt aag aaa 1587
158 Ala Tyr Gly Tyr Arg Lys Cys Leu Gly Lys Lys Gly Arg Val Lys Lys
159 510 515 520
161 gcc cac aaa tcc aag acc cat tga gaagtgggtg ggaaataagg taaaattttg 1641
162 Ala His Lys Ser Lys Thr His
163 525 530
165 aaccattccc tagtcatttc caaacttgaa aacagaatca gtgttaaatt cattttattc 1701
167 ttattaagga aatactttgc ataaattaat cagcccccaga gtgctttaa aaattctott 1761
169 aaataaaaaat aatagactcg ctagtgcagta aagatatttg aatatgtatc gtgccccctc 1821
171 cggtgtcttt gatcaggatg acatgtgcca tttttcagag gacgtgcaga caggctggca 1881
173 ttctagatta cttttcttac tctgaaacat ggcctgtttg ggagtgcggg attcaaagggt 1941
175 ggtcccaccg ctgcccctac tgcaaatggc agttttaato ttatcttttg gcttctgcag 2001
177 atgggtgcaa ttgatcctta accaataatg gtcagtcctc atctctgtcc tgcttcatag 2061
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181 atgaatggct tggagtgcac tgagaacagc atatgatttc ttgctttggg gaaaaagaat 2181
183 gatgctatga aattgggtggg tgggtgtattt gagaagataa tcattgctta tgtcaaatgg 2241
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199 20 25 30
200 Met Asp Gly Ser His Trp Phe Thr Met Arg Ser Val Val Glu Lys Leu
201 35 40 45
202 Ile Leu Arg Gly His Glu Val Val Val Val Met Pro Glu Val Ser Trp
203 50 55 60

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204 Gln Leu Gly Arg Ser Leu Asn Cys Thr Val Lys Thr Tyr Ser Thr Ser
205 65 70 75 80
206 Tyr Thr Leu Glu Asp Leu Asp Arg Glu Phe Lys Ala Phe Ala His Ala
207 85 90 95
208 Gln Trp Lys Ala Gln Val Arg Ser Ile Tyr Ser Leu Leu Met Gly Ser
209 100 105 110
210 Tyr Asn Asp Ile Phe Asp Leu Phe Phe Ser Asn Cys Arg Ser Leu Phe
211 115 120 125
212 Lys Asp Lys Lys Leu Val Glu Tyr Leu Lys Glu Ser Ser Phe Asp Ala
213 130 135 140
214 Val Phe Leu Asp Pro Phe Asp Asn Cys Gly Leu Ile Val Ala Lys Tyr
215 145 150 155 160
216 Phe Ser Leu Pro Ser Val Val Phe Ala Arg Gly Ile Leu Cys His Tyr
217 165 170 175
218 Leu Glu Glu Gly Ala Gln Cys Pro Ala Pro Leu Ser Tyr Val Pro Arg
219 180 185 190
220 Ile Leu Leu Gly Phe Ser Asp Ala Met Thr Phe Lys Glu Arg Val Arg
221 195 200 205
222 Asn His Ile Met His Leu Glu Glu His Leu Leu Cys His Arg Phe Phe
223 210 215 220
224 Lys Asn Ala Leu Glu Ile Ala Ser Glu Ile Leu Gln Thr Pro Val Thr
225 225 230 235 240
226 Glu Tyr Asp Leu Tyr Ser His Thr Ser Ile Trp Leu Leu Arg Thr Asp
227 245 250 255
228 Phe Val Leu Asp Tyr Pro Lys Pro Val Met Pro Asn Met Ile Phe Ile
229 260 265 270
230 Gly Gly Ile Asn Cys His Gln Gly Lys Pro Leu Pro Met Glu Phe Glu
231 275 280 285
232 Ala Tyr Ile Asn Ala Ser Gly Glu His Gly Ile Val Val Phe Ser Leu
233 290 295 300
234 Gly Ser Met Val Ser Glu Ile Pro Glu Lys Lys Ala Met Ala Ile Ala
235 305 310 315 320
236 Asp Ala Leu Gly Lys Ile Pro Gln Thr Val Leu Trp Arg Tyr Thr Gly
237 325 330 335
238 Thr Arg Pro Ser Asn Leu Ala Asn Asn Thr Ile Leu Val Lys Trp Leu
239 340 345 350
240 Pro Gln Asn Asp Leu Leu Gly His Pro Met Thr Arg Ala Phe Ile Thr
241 355 360 365
242 His Ala Gly Ser His Gly Val Tyr Glu Ser Ile Cys Asn Gly Val Pro
243 370 375 380
244 Met Val Met Met Pro Leu Phe Gly Asp Gln Met Asp Asn Ala Lys Arg
245 385 390 395 400
246 Met Glu Thr Lys Gly Ala Gly Val Thr Leu Asn Val Leu Glu Met Thr
247 405 410 415
248 Ser Glu Asp Leu Glu Asn Ala Leu Lys Ala Val Ile Asn Asp Lys Ser
249 420 425 430
250 Tyr Lys Glu Asn Ile Met Arg Leu Ser Ser Leu His Lys Asp Arg Pro
251 435 440 445
252 Val Glu Pro Leu Asp Leu Ala Val Phe Trp Val Glu Phe Val Met Arg

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253      450      455      460
254 His Lys Gly Ala Pro His Leu Arg Pro Ala Ala His Asp Leu Thr Trp
255 465      470      475      480
256 Tyr Gln Tyr His Ser Leu Asp Val Ile Gly Phe Leu Leu Ala Val Val
257      485      490      495
258 Leu Thr Val Ala Phe Ile Thr Phe Lys Cys Cys Ala Tyr Gly Tyr Arg
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260 Lys Cys Leu Gly Lys Lys Gly Arg Val Lys Lys Ala His Lys Ser Lys
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262 Thr His
263      530
266 <210> SEQ ID NO: 3
267 <211> LENGTH: 2320
268 <212> TYPE: DNA
269 <213> ORGANISM: Homo sapiens
271 <220> FEATURE:
272 <221> NAME/KEY: CDS
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280 cta tgt gtg tgt ctg ctg ctg acc tgt ggc ttt gcc gag gca ggg aag 99
281 Leu Cys Val Cys Leu Leu Leu Thr Cys Gly Phe Ala Glu Ala Gly Lys
282      15      20      25
284 cta ctg gta gtg ccc atg gat ggg agc cac tgg ttc acc atg agg tcg 147
285 Leu Leu Val Val Pro Met Asp Gly Ser His Trp Phe Thr Met Arg Ser
286      30      35      40
288 gtg gtg gag aaa ctc att ctc agg ggg cat gag gtg gtt gta gtc atg 195
289 Val Val Glu Lys Leu Ile Leu Arg Gly His Glu Val Val Val Met
290      45      50      55
292 cca gag gtg agt tgg caa ctg gga aga tca ctg aat tgc aca gtg aag 243
293 Pro Glu Val Ser Trp Gln Leu Gly Arg Ser Leu Asn Cys Thr Val Lys
294      60      65      70      75
296 act tat tca act tca tat acc ctg gag gat ctg gac cgg gag ttc aag 291
297 Thr Tyr Ser Thr Ser Tyr Thr Leu Glu Asp Leu Asp Arg Glu Phe Lys
298      80      85      90
300 gct ttt gcc cat gct caa tgg aaa gca caa gta cga agt ata tat tct 339
301 Ala Phe Ala His Ala Gln Trp Lys Ala Gln Val Arg Ser Ile Tyr Ser
302      95      100      105
304 cta tta atg ggt tca tac aat gac att ttt gac tta ttt ttt tca aat 387
305 Leu Leu Met Gly Ser Tyr Asn Asp Ile Phe Asp Leu Phe Phe Ser Asn
306      110      115      120
308 tgc agg agt ttg ttt aaa gac aaa aaa tta gta gaa tac tta aag gag 435
309 Cys Arg Ser Leu Phe Lys Asp Lys Lys Leu Val Glu Tyr Leu Lys Glu
310      125      130      135
312 agt tct ttt gat gca gtg ttt ctc gat cct ttt gat aac tgt ggc tta 483
313 Ser Ser Phe Asp Ala Val Phe Leu Asp Pro Phe Asp Asn Cys Gly Leu
314 140      145      150      155

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VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number